SEQUENCE LISTING

<110> Labas, Yulii Aleksandrovich
Gurskaya, Nadezda Georgievna
Yanushevich, Yuriy
Fradkov, Arcady Fedorovich
Lukyanov, Konstantin
Lukyanov, Sergey
Matz, Mikhail Vladimirovich

<120> NOVEL CHROMOPHORES/FLUOROPHORES AND METHODS FOR USING THE SAME

<130> CLON-090

<140> 10/757,356
<141> 2004-01-13

<150> 60/332,980
<151> 2001-11-13

<150> PCT/US02/36499
<151> 2002-11-12

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<213> Heteractis crispa

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agcctgacga tcaccgtaac tgaaggaggt cctctgccat ttgccttcga cattctttca 240
cacgcctttc gatatggcaa taaggtgttc gccaagtacc ccaaagatca tcctgatttt 300
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cccgcactga agctgcttgg taacaaagga catcttctct gcgtcatgga aacaacttac 600
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gatagtgtta gtgacgatga gaagaccatt gagcagcacg agaatgtgag ggcaagctac 720
ttcaatgata gtggaaaatg atcatttcct tattgatttc aatgttaggg cattcagttt 780
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<210> 2
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<213> Heteractis crispa

<400> 2

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            20                  25                  30
Glu Pro Tyr Lys Gly Ser Gln Ser Leu Thr Ile Thr Val Thr Glu Gly
        35                  40                  45
Gly Pro Leu Pro Phe Ala Phe Asp Ile Leu Ser His Ala Phe Arg Tyr
    50                  55                  60
Gly Asn Lys Val Phe Ala Lys Tyr Pro Lys Asp His Pro Asp Phe Phe
65                  70                  75                  80
Lys Gln Ser Leu Pro Glu Gly Phe Thr Trp Glu Arg Val Ser Asn Tyr
                85                  90                  95
Glu Asp Gly Gly Val Leu Thr Val Lys Gln Glu Thr Ser Leu Glu Gly
            100                 105                 110
Asp Cys Ile Ile Cys Lys Ile Lys Ala His Gly Thr Asn Phe Pro Ala
        115                 120                 125
Asp Gly Pro Val Met Gln Lys Arg Thr Asn Gly Trp Glu Pro Ser Thr
    130                 135                 140
Glu Thr Val Ile Pro Arg Gly Gly Gly Ile Leu Met Arg Asp Val Pro
145                 150                 155                 160
Ala Leu Lys Leu Leu Gly Asn Lys Gly His Leu Leu Cys Val Met Glu
                165                 170                 175
Thr Thr Tyr Lys Ser Lys Lys Lys Gly Glu Pro Ala Lys Pro His Phe
            180                 185                 190
His His Leu Arg Met Glu Lys Asp Ser Val Ser Asp Asp Glu Lys Thr
        195                 200                 205
Ile Glu Gln His Glu Asn Val Arg Ala Ser Tyr Phe Asn Asp Ser Gly
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225
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<213> Dendronephthya sp

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attgaagggg aaggaaaagg aaggccctac gaagggacac agaccttgaa cctgacagtg 180
aaagaaggcg cgcctctccc attttcttac gacatcttga caacagcatt gcactacgga 240
aacagagtat tcactgaata cccagcagat atcacggatt atttcaagca atcatttcct 300
gaaggatatt cctgggaaag aaccatgact tatgaagaca agggcatttg taccatcaga 360
agcgacataa gcttggaagg tgactgcttt ttccaaaaca ttcgttttaa tgggatgaac 420
tttccccca atggtccagt tatgcagaag aaaactttga agtgggaacc atccacagag 480
aagctgcacg tgcgtgatgg gttgcttgtc ggtaatatta acatggctct gctgcttgaa 540
ggaggtggac attacctgtg tgacttcaaa actacttaca aagcgaagaa ggttgttcag 600
ttgccagatt atcattttgt ggaccatcgc attgagatct tgagtaatga cagcgattac 660
aacaaagtga agctgtacga gcatggggtt gctcgctatt ctccgttgcc caagtcaggc 720
ctggtagagg ttcaagggaa agccataatg actgcataga taaacatgta gtgaagacca 780
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<212> PRT
<213> Dendronephthya sp

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            20   25   30
Pro Tyr Glu Gly Thr Gln Thr Leu Asn Leu Thr Val Lys Glu Gly Ala
        35   40   45
Pro Leu Pro Phe Ser Tyr Asp Ile Leu Thr Thr Ala Leu His Tyr Gly
    50   55   60
Asn Arg Val Phe Thr Glu Tyr Pro Ala Asp Ile Thr Asp Tyr Phe Lys
65   70   75   80
Gln Ser Phe Pro Glu Gly Tyr Ser Trp Glu Arg Thr Met Thr Tyr Glu
                85   90   95
Asp Lys Gly Ile Cys Thr Ile Arg Ser Asp Ile Ser Leu Glu Gly Asp
            100   105   110
Cys Phe Phe Gln Asn Ile Arg Phe Asn Gly Met Asn Phe Pro Pro Asn
        115   120   125
Gly Pro Val Met Gln Lys Lys Thr Leu Lys Trp Glu Pro Ser Thr Glu
    130   135   140
Lys Leu His Val Arg Asp Gly Leu Leu Val Gly Asn Ile Asn Met Ala
145   150   155   160
Leu Leu Leu Glu Gly Gly Gly His Tyr Leu Cys Asp Phe Lys Thr Thr
                165   170   175
Tyr Lys Ala Lys Lys Val Val Gln Leu Pro Asp Tyr His Phe Val Asp
            180   185   190
His Arg Ile Glu Ile Leu Ser Asn Asp Ser Asp Tyr Asn Lys Val Lys
        195   200   205
Leu Tyr Glu His Gly Val Ala Arg Tyr Ser Pro Leu Pro Lys Ser Gly
    210   215   220
Leu Val Glu Val Gln Gly Lys Ala Ile Met Thr Ala
225   230   235

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<211> 851
<212> DNA
<213> Zoanthus sp

<400> 5
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tgcgtcgatg gacataagtt tgtaatcgag ggcaacggca atggaaatcc tttcaaaggg 180
aaacagttta ttaatctgtg tgtgattgaa ggaggaccac tgccattctc cgaagacata 240
ttgtctgctg cgtttgacta cggaaacagg ctcttcactg aatatcctga aggcatagtt 300
gactatttca agaactcgtg tcctgctgga tatacgtggc acaggtcttt tcgctttgaa 360
gatggagcag tttgcatatg cagtgcagat ataacagtaa atgttaggga aaactgcatt 420
tatcatgagt ccacgtttta tggagtgaac tttcctgctg atggacctgt gatgaaaaag 480
atgacaacta attgggaacc gtcctgcgag aaaatcatac caataaatag tcagaagata 540
ttaaaagggg atgtctccat gtacctcctt ctgaaggatg gtgggcgtta ccgctgccag 600
tttgacacaa tttacaaagc aaagactgag ccaaaagaaa tgccggactg gcacttcatc 660
cagcataagc tcaaccgtga agaccgcagc gatgctaaga atcagaaatg gcaactgata 720
gaacatgcta ttgcatcccg atctgcttta ccctgataac aaaggagttg ctattgcatg 780
tgcatgccta ttacgctgat aaaaatgtag ttttaacatg caattgtatg tgcatgcaca 840
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<210> 6
<211> 231

<212> PRT
<213> Zoanthus sp

<400> 6
Met Ala His Ser Lys His Gly Leu Thr Asp Asp Met Thr Met His Phe
 1   5   10   15
Arg Met Glu Gly Cys Val Asp Gly His Lys Phe Val Ile Glu Gly Asn
            20   25   30
Gly Asn Gly Asn Pro Phe Lys Gly Lys Gln Phe Ile Asn Leu Cys Val
        35   40   45
Ile Glu Gly Gly Pro Leu Pro Phe Ser Glu Asp Ile Leu Ser Ala Ala
    50   55   60
Phe Asp Tyr Gly Asn Arg Leu Phe Thr Glu Tyr Pro Glu Gly Ile Val
65   70   75   80
Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp His Arg Ser
                85   90   95
Phe Arg Phe Glu Asp Gly Ala Val Cys Ile Cys Ser Ala Asp Ile Thr
            100   105   110
Val Asn Val Arg Glu Asn Cys Ile Tyr His Glu Ser Thr Phe Tyr Gly
        115   120   125
Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Met Thr Thr Asn
    130   135   140
Trp Glu Pro Ser Cys Glu Lys Ile Ile Pro Ile Asn Ser Gln Lys Ile
145   150   155   160
Leu Lys Gly Asp Val Ser Met Tyr Leu Leu Leu Lys Asp Gly Gly Arg
                165   170   175
Tyr Arg Cys Gln Phe Asp Thr Ile Tyr Lys Ala Lys Thr Glu Pro Lys
            180   185   190
Glu Met Pro Asp Trp His Phe Ile Gln His Lys Leu Asn Arg Glu Asp
        195   200   205
Arg Ser Asp Ala Lys Asn Gln Lys Trp Gln Leu Ile Glu His Ala Ile
    210   215   220
Ala Ser Arg Ser Ala Leu Pro
225   230

<210> 7
<211> 1178
<212> DNA
<213> Scolymia cubensis

<400> 7
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ttggacggga gcagatcgag aacaacmagg gctgtacgag tctgataatt tactttacat 120
ctaccaacat gcagcgtgct gggatgaagg ttaaggaaca tatgaagatc aaactgcgta 180
tgggaggtac tgtaaacgga aagcatttcg cggttaatgg gacaggagac ggctaccctt 240
atcagggaaa acagattttg aaacttatcg tcgaaggcag cgaacctctg cctttcgctt 300
ttgatatctt gtcagcagca ttccagtatg gcaacagggc attcaccgaa tacccaacag 360
agatagcaga ctatttcaag cagtcgtttg agtttggcga ggggttctcc tgggaacgaa 420
gtttcacttt cgaagatggg gccatttgcg tcgccaccaa cgatataacg atggttggtg 480
gtgagtttca gtatgatatt cgatttgatg gtctgaactt ccctgaagat ggtccagtga 540
tgcaaaagaa aaccgtaaaa tgggagccat ccactgagat aatgtatatg caaaatggag 600
tgctgaaggg tgaggttaac atggctctgt tgcttcaaga caaaagccat taccgttgcg 660
acctcaaaac tacttacaaa gctaagaata atgtgccgca tcctccaggc taccactatg 720
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ctaaagctcg ttctagcctg tcacctacca gtgcaaaaga acgaaaggct taggtgatag 840
tcaaaaagac aacaagacga aaatgaaagg tgttcattgt tagaatttga tattttcgat 900
tcaatgattc gttaagggat ttgctagagg ctagctaaca ggttaacatc ataaggatag 960

agattycgtt gcggagttag aaccttwata ttttccgaat tccamctaga gtcgttgaga 1020
aatttattag agactagctt tagagttact tttgtggaaa aaaaggtttc cattttttgc 1080
gttattacag catttaaagc ataggaatag agattcggtt atggaaaata acagtaggaa 1140
aatacgttgt gaaaataaac ttgttgtcga aaaaaaaa 1178

<210> 8
<211> 234
<212> PRT
<213> Scolymia cubensis

<400> 8
Met Gln Arg Ala Gly Met Lys Val Lys Glu His Met Lys Ile Lys Leu
 1   5   10   15
Arg Met Gly Gly Thr Val Asn Gly Lys His Phe Ala Val Asn Gly Thr
            20   25   30
Gly Asp Gly Tyr Pro Tyr Gln Gly Lys Gln Ile Leu Lys Leu Ile Val
        35   40   45
Glu Gly Ser Glu Pro Leu Pro Phe Ala Phe Asp Ile Leu Ser Ala Ala
    50   55   60
Phe Gln Tyr Gly Asn Arg Ala Phe Thr Glu Tyr Pro Thr Glu Ile Ala
65   70   75   80
Asp Tyr Phe Lys Gln Ser Phe Glu Phe Gly Glu Gly Phe Ser Trp Glu
                85   90   95
Arg Ser Phe Thr Phe Glu Asp Gly Ala Ile Cys Val Ala Thr Asn Asp
            100   105   110
Ile Thr Met Val Gly Gly Glu Phe Gln Tyr Asp Ile Arg Phe Asp Gly
        115   120   125
Leu Asn Phe Pro Glu Asp Gly Pro Val Met Gln Lys Lys Thr Val Lys
    130   135   140
Trp Glu Pro Ser Thr Glu Ile Met Tyr Met Gln Asn Gly Val Leu Lys
145   150   155   160
Gly Glu Val Asn Met Ala Leu Leu Leu Gln Asp Lys Ser His Tyr Arg
                165   170   175
Cys Asp Leu Lys Thr Thr Tyr Lys Ala Lys Asn Asn Val Pro His Pro
            180   185   190
Pro Gly Tyr His Tyr Val Asp His Cys Ile Glu Ile Leu Glu Glu Arg
        195   200   205
Lys Asp His Val Lys Leu Arg Glu His Ala Lys Ala Arg Ser Ser Leu
    210   215   220
Ser Pro Thr Ser Ala Lys Glu Arg Lys Ala
225   230

<210> 9
<211> 819
<212> DNA
<213> Scolymia cubensis

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gatcacactg cgtatggacg gtgctgtaaa cgggaagccc ttcgcggtta atggaacagg 180
agatggcaac ccttatggtg gaatacagag tttgaagctt accgtcgatg gcaacaaacc 240
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cgaataccca aaagagatat cagactattt caagcagtcg tttgagtttg gcgaggggtt 360
tacctgggaa cgaagtttca ctttcgaaga cggggccatt tgcgtcgcca cgaacgatat 420
aaagatggtt ggcgatgagt ttcaatataa cattcgattt gatggtgtga atttccctga 480
agatggtccw gtyatgcaga agaaaacggt gaagtgggag ccatccacag agataatgcg 540

tgtgcaaggt ggagtgctaa agggtgaggt taacatggct ctgttgctta aagacaaaag 600
ccattaccga tgtgacttca aaactactta caaagctaag aatcctgtcc cgccgacggc 660
gcttccagac taccactatg tggatcactg tattgaaatc accgaggaaa atagggatta 720
cgttaagctg caggagtatg ctaaagctcg ttctggcctg cacctgcccg aactgcaaaa 780
gtaaaggctt aggcgatagt caagacgaca acgagaaga 819

<210> 10
<211> 235
<212> PRT
<213> Scolymia cubensis

<400> 10
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Thr Leu Arg Met Asp Gly Ala Val Asn Gly Lys Pro Phe Ala Val Asn
            20   25   30
Gly Thr Gly Asp Gly Asn Pro Tyr Gly Gly Ile Gln Ser Leu Lys Leu
        35   40   45
Thr Val Asp Gly Asn Lys Pro Leu Pro Phe Ala Phe Asp Ile Leu Ser
    50   55   60
Ala Ala Phe Gln Tyr Gly Asn Arg Ala Phe Thr Glu Tyr Pro Lys Glu
65   70   75   80
Ile Ser Asp Tyr Phe Lys Gln Ser Phe Glu Phe Gly Glu Gly Phe Thr
                85   90   95
Trp Glu Arg Ser Phe Thr Phe Glu Asp Gly Ala Ile Cys Val Ala Thr
            100   105   110
Asn Asp Ile Lys Met Val Gly Asp Glu Phe Gln Tyr Asn Ile Arg Phe
        115   120   125
Asp Gly Val Asn Phe Pro Glu Asp Gly Pro Val Met Gln Lys Lys Thr
    130   135   140
Val Lys Trp Glu Pro Ser Thr Glu Ile Met Arg Val Gln Gly Gly Val
145   150   155   160
Leu Lys Gly Glu Val Asn Met Ala Leu Leu Leu Lys Asp Lys Ser His
                165   170   175
Tyr Arg Cys Asp Phe Lys Thr Thr Tyr Lys Ala Lys Asn Pro Val Pro
            180   185   190
Pro Thr Ala Leu Pro Asp Tyr His Tyr Val Asp His Cys Ile Glu Ile
        195   200   205
Thr Glu Glu Asn Arg Asp Tyr Val Lys Leu Gln Glu Tyr Ala Lys Ala
    210   215   220
Arg Ser Gly Leu His Leu Pro Glu Leu Gln Lys
225   230   235

<210> 11
<211> 807
<212> DNA
<213> Ricordea florida

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aaatcaagct tacattggtg ggcgttgtta acgggcaccc attcaagatc attggggacg 120
gaaaaggcaa accctatgag ggatcgcagg aattaaccct tgccgtggtg gaaggagggc 180
ctctgccttt ctcttatgat atcctgacaa cgatagttca ctatggcaac agggcatttg 240
tgaactaccc aaaggacata ccagatattt tcaagcagac ctgctctggt cctggtgctg 300
gatattcctg gcaaaggacc atgagttttg aagacggagg cgtttgcact gctacgagcc 360
atatcagggt ggatggcgac actttcaatt atgacattca cttcatggga gcggatttcc 420
ctcttaatgg tccagtgatg cagaaaagaa cagtgaaatg ggagccatcc actgagataa 480

tgtttcaatg tgatggattg ctgaggggtg atgttgccat gtctctgttg ctgaaaggag 540
gcggccatta ccgatgtgac tttaaaacta tttataaacc caagaagaat gtcaagatgc 600
caggttacca ttttgtggac cactgcattg agataacgag tcaacaggac gattacaacg 660
tggttgagct gtacgagggt gctgtagccc actactctcc tctgcagaaa ccatgccaag 720
caaaggcata aagccaaaca acccaagagg acaacaagac atttaatcaa atcacatctt 780
tgtatttttg gttagagttg aaaaaaa 807

<210> 12
<211> 231
<212> PRT
<213> Ricordea florida

<400> 12
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 1   5   10   15
Val Val Asn Gly His Pro Phe Lys Ile Ile Gly Asp Gly Lys Gly Lys
            20   25   30
Pro Tyr Glu Gly Ser Gln Glu Leu Thr Leu Ala Val Val Glu Gly Gly
        35   40   45
Pro Leu Pro Phe Ser Tyr Asp Ile Leu Thr Thr Ile Val His Tyr Gly
    50   55   60
Asn Arg Ala Phe Val Asn Tyr Pro Lys Asp Ile Pro Asp Ile Phe Lys
65   70   75   80
Gln Thr Cys Ser Gly Pro Gly Ala Gly Tyr Ser Trp Gln Arg Thr Met
                85   90   95
Ser Phe Glu Asp Gly Gly Val Cys Thr Ala Thr Ser His Ile Arg Val
            100   105   110
Asp Gly Asp Thr Phe Asn Tyr Asp Ile His Phe Met Gly Ala Asp Phe
        115   120   125
Pro Leu Asn Gly Pro Val Met Gln Lys Arg Thr Val Lys Trp Glu Pro
    130   135   140
Ser Thr Glu Ile Met Phe Gln Cys Asp Gly Leu Leu Arg Gly Asp Val
145   150   155   160
Ala Met Ser Leu Leu Leu Lys Gly Gly Gly His Tyr Arg Cys Asp Phe
                165   170   175
Lys Thr Ile Tyr Lys Pro Lys Lys Asn Val Lys Met Pro Gly Tyr His
            180   185   190
Phe Val Asp His Cys Ile Glu Ile Thr Ser Gln Gln Asp Asp Tyr Asn
        195   200   205
Val Val Glu Leu Tyr Glu Gly Ala Val Ala His Tyr Ser Pro Leu Gln
    210   215   220
Lys Pro Cys Gln Ala Lys Ala
225   230

<210> 13
<211> 796
<212> DNA
<213> Ricordea florida

<400> 13
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taaaatggtg ggcgttgtta acgggcagtc atttcagatc gatggggaag gaaaaggcaa 180
accttacgag ggatcacaga aattaaccct tgaagtggtg gaaggagggc ctctgctctt 240
ctcttatgat atcctgacaa cgatatttca gtatggcaac agggcattcg tgaactaccc 300
aaaggacata ccagatattt tcaagcagac ctgctctggt cctgatggtg gattttcctg 360
gcaaaggacc atgacttatg aagacggagg ggtttgcact gcttcaaacc acatcagcgt 420

ggacggcgac actttttatt atgtgataag atttaatgga gagaattttc ctccaaatgg 480
tccagtaatg cagaaaagaa cagtgaaatg ggagccatcc actgagataa tgtttgaacg 540
tgatggattg ctgaggggtg acattgccat gtctctgttg ctgaaaggag gcggccatta 600
ccgatgtgac tttaaaacta tttatacacc caagaggaag gtcaacatgc caggttacca 660
ttttgtggac cactgcattg agatacagaa gcacgacaag gattacaaca tggctgtgct 720
ctctgaggat gctgtagccc acaactctcc tctggagaaa aaaagccaag caaaggcgta 780
aagccaaaca acctaa 796

<210> 14
<211> 231
<212> PRT
<213> Ricordea florida

<400> 14
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Val Val Asn Gly Gln Ser Phe Gln Ile Asp Gly Glu Gly Lys Gly Lys
            20   25   30
Pro Tyr Glu Gly Ser Gln Lys Leu Thr Leu Glu Val Val Glu Gly Gly
        35   40   45
Pro Leu Leu Phe Ser Tyr Asp Ile Leu Thr Thr Ile Phe Gln Tyr Gly
    50   55   60
Asn Arg Ala Phe Val Asn Tyr Pro Lys Asp Ile Pro Asp Ile Phe Lys
65   70   75   80
Gln Thr Cys Ser Gly Pro Asp Gly Gly Phe Ser Trp Gln Arg Thr Met
                85   90   95
Thr Tyr Glu Asp Gly Gly Val Cys Thr Ala Ser Asn His Ile Ser Val
            100   105   110
Asp Gly Asp Thr Phe Tyr Tyr Val Ile Arg Phe Asn Gly Glu Asn Phe
        115   120   125
Pro Pro Asn Gly Pro Val Met Gln Lys Arg Thr Val Lys Trp Glu Pro
    130   135   140
Ser Thr Glu Ile Met Phe Glu Arg Asp Gly Leu Leu Arg Gly Asp Ile
145   150   155   160
Ala Met Ser Leu Leu Leu Lys Gly Gly Gly His Tyr Arg Cys Asp Phe
                165   170   175
Lys Thr Ile Tyr Thr Pro Lys Arg Lys Val Asn Met Pro Gly Tyr His
            180   185   190
Phe Val Asp His Cys Ile Glu Ile Gln Lys His Asp Lys Asp Tyr Asn
        195   200   205
Met Ala Val Leu Ser Glu Asp Ala Val Ala His Asn Ser Pro Leu Glu
    210   215   220
Lys Lys Ser Gln Ala Lys Ala
225   230

<210> 15
<211> 795
<212> DNA
<213> Montastraea cavernosa

<400> 15
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caagctgcgt atggaaggca gtgtaaacgg gcacaacttc gtaattgttg gagaaggaga 180
aggcaagcct tatgagggaa cacagagtat ggaccttaca gtcaaagaag gcgcacctct 240
gcctttcgcc tacgatatca tgacaacagt attccattac ggcaataggg tattcgcaaa 300
atacccaaaa catatcccag actatttcaa gcagatgttt cctgaggagt attcctggga 360

acgaagcatg aatttcgaag gcgggggcat ttgcaccgcc aggaacgaga taacaatgga 420
aggcgactgt tttttcaata aagttcgatt tgatggtgtg aacttccccc ccaatggtcc 480
agtcatgcag aagaagacgc tgaaatggga gccatccact gaaaaaatgt atgtgcgtga 540
tggagtgctg acgggtgata tcaacatggc tttgttgctt gaaggaggtg gccattaccg 600
atgtgacttc agaactactt acagagctaa gaagaagggt gtcaagttac cagattatca 660
ctttgaggat cactccattg agattttgcg ccatgacaaa gaatacactg aggttaagct 720
gtatgagcat gccgaagctc attctgggct gccgagggtg gcaaagtaaa ggcttaacga 780
aaagccaaga ccaca 795

<210> 16
<211> 235
<212> PRT
<213> Montastraea cavernosa

<400> 16
Arg Leu Ile Ser Tyr Phe Thr Ser Thr Ile Met Ser Val Ile Lys Ser
 1   5   10   15
Val Met Lys Ile Lys Leu Arg Met Glu Gly Ser Val Asn Gly His Asn
            20   25   30
Phe Val Ile Val Gly Glu Gly Glu Gly Lys Pro Tyr Glu Gly Thr Gln
        35   40   45
Ser Met Asp Leu Thr Val Lys Glu Gly Ala Pro Leu Pro Phe Ala Tyr
    50   55   60
Asp Ile Met Thr Thr Val Phe His Tyr Gly Asn Arg Val Phe Ala Lys
65   70   75   80
Tyr Pro Lys His Ile Pro Asp Tyr Phe Lys Gln Met Phe Pro Glu Glu
                85   90   95
Tyr Ser Trp Glu Arg Ser Met Asn Phe Glu Gly Gly Gly Ile Cys Thr
            100   105   110
Ala Arg Asn Glu Ile Thr Met Glu Gly Asp Cys Phe Phe Asn Lys Val
        115   120   125
Arg Phe Asp Gly Val Asn Phe Pro Pro Asn Gly Pro Val Met Gln Lys
    130   135   140
Lys Thr Leu Lys Trp Glu Pro Ser Thr Glu Lys Met Tyr Val Arg Asp
145   150   155   160
Gly Val Leu Thr Gly Asp Ile Asn Met Ala Leu Leu Leu Glu Gly Gly
                165   170   175
Gly His Tyr Arg Cys Asp Phe Arg Thr Thr Tyr Arg Ala Lys Lys Lys
            180   185   190
Gly Val Lys Leu Pro Asp Tyr His Phe Glu Asp His Ser Ile Glu Ile
        195   200   205
Leu Arg His Asp Lys Glu Tyr Thr Glu Val Lys Leu Tyr Glu His Ala
    210   215   220
Glu Ala His Ser Gly Leu Pro Arg Val Ala Lys
225   230   235

<210> 17
<211> 1066
<212> DNA
<213> Montastraea cavernosa

<400> 17
attcgccctg gtgatttgga agagagcaga tcgagaacaa caagagctgt aaggttgata 60
tcttacttac gtctaccatc atgacaagtg ttgcacagga aaagggtgtg attaaaccag 120
acatgaagat gaagctgcgt atggaaggtg ctgtaaacgg gcacaagttc gtggttgaag 180
gagatggaaa agggaagcct ttcgacggaa cacagactat ggaccttaca gtcatagaag 240
gcgcaccatt gcctttcgct tacgatatct tgacaacagt attcgattac ggcaacaggg 300

tattcgccaa atacccagaa gacatagcag attatttcaa gcagacgttt cctgaggggt 360
acttctggga acgaagcatg acatacgaag accagggcat ttgcatcgcc acaaacgaca 420
taacaatgat ggaaggcgtc gacgactgtt ttgcctataa aattcgattt gatggtgtga 480
actttcctgc caatggtcca gttatgcaga ggaagacgct gaaatgggag ccatccactg 540
agataatgta tgcgcgtgat ggagtgctga agggtgatgt taacatggct ctgttgcttg 600
aaggaggtgg ccattaccga tgtgacttca aaactactta caaagctaag aaggttgtcc 660
ggttgccaga ctatcacttt gtggaccatc gcattgagat tgtgagccac gacaaagatt 720
acaacaaggt taagctgcac gagcatgccg aagctcgtca tggactgtca aggaaggcca 780
agtaaaggct taatgaaaag tcaagacgac aacgaggaga aacaaagtac ttttttgtta 840
aatttgaagg catttactcg gaattagtat ttgatacttt cgattcaagg atttgttccg 900
ggatttgtta gagactagct ctagagttgt attttgtgaa aaaagatagt ttccagtttt 960
tgcgggatta cagcatgggg atagactttt taaactcagt tgtggtcaaa tgcaagtaag 1020
aaaactgtag tgagaataaa cttgttatcg aagccgaaaa aaaaaa 1066

<210> 18
<211> 234
<212> PRT
<213> Montastraea cavernosa

<400> 18
Met Thr Ser Val Ala Gln Glu Lys Gly Val Ile Lys Pro Asp Met Lys
 1   5   10   15
Met Lys Leu Arg Met Glu Gly Ala Val Asn Gly His Lys Phe Val Val
            20   25   30
Glu Gly Asp Gly Lys Gly Lys Pro Phe Asp Gly Thr Gln Thr Met Asp
        35   40   45
Leu Thr Val Ile Glu Gly Ala Pro Leu Pro Phe Ala Tyr Asp Ile Leu
    50   55   60
Thr Thr Val Phe Asp Tyr Gly Asn Arg Val Phe Ala Lys Tyr Pro Glu
65   70   75   80
Asp Ile Ala Asp Tyr Phe Lys Gln Thr Phe Pro Glu Gly Tyr Phe Trp
                85   90   95
Glu Arg Ser Met Thr Tyr Glu Asp Gln Gly Ile Cys Ile Ala Thr Asn
            100   105   110
Asp Ile Thr Met Met Glu Gly Val Asp Asp Cys Phe Ala Tyr Lys Ile
        115   120   125
Arg Phe Asp Gly Val Asn Phe Pro Ala Asn Gly Pro Val Met Gln Arg
    130   135   140
Lys Thr Leu Lys Trp Glu Pro Ser Thr Glu Ile Met Tyr Ala Arg Asp
145   150   155   160
Gly Val Leu Lys Gly Asp Val Asn Met Ala Leu Leu Leu Glu Gly Gly
                165   170   175
Gly His Tyr Arg Cys Asp Phe Lys Thr Thr Tyr Lys Ala Lys Lys Val
            180   185   190
Val Arg Leu Pro Asp Tyr His Phe Val Asp His Arg Ile Glu Ile Val
        195   200   205
Ser His Asp Lys Asp Tyr Asn Lys Val Lys Leu His Glu His Ala Glu
    210   215   220
Ala Arg His Gly Leu Ser Arg Lys Ala Lys
225   230

<210> 19
<211> 898
<212> DNA
<213> Condylactis gigantea

<400> 19

acagctgttc atccacgctc attcaagacg ccgtcaactt tattccagtc aggaaaatgt 60
atccttggat caaggaaacc atgcgcagta aggtttacat ggaaggagat gttaacaacc 120
acgccttcaa gtgcactgca gtaggagaag gaaaaccata caaaggctca caagacctga 180
cgattaccgt cactgaagga ggtcctctgc catttgcttt cgacattctt tcacacgcct 240
ttcagtatgg caacaaggtg ttcaccgatt accccgacga tattcctgat ttctttaagc 300
agtctctctc ggatggtttt acttggagaa gagtaagcac statgacgat ggaggagtcc 360
tcacagttac ccaagacact agtctgaagg gagattgcat tatttgcaac attaaagtcc 420
atggcactaa cttccccgaa aatggtccgg tgatgcaaaa caagaccgat ggatgggagc 480
catccagcac tgaaacggtt attccacaag atggaggaat tgttgctgcg cgatcacccg 540
cactaaggct gcgtgataaa ggtcatctta tctgccacat ggaaacaact tacaagccaa 600
acaaagaggt gaagctgcca gaactccact ttcatcattt gcgaatggaa aagctgagtg 660
ttagtgacga tgggaagacc attaagcagc acgagtatgt ggtggctagc tactccaaag 720
tgccttcgaa gataggacgt caatgatcat ttcccttatt aaatatcaat gatgtggctt 780
tcaattttcc aaaattttgt taagacatag gtcttttgga tttttggtaa ccccaacctt 840
aattcccaat aatttttgtt ggaaagtcaa ataaaaccag ccttccctgg gcctttaa 898

<210> 20
<211> 229
<212> PRT
<213> Condylactis gigantea

<400> 20
Met Tyr Pro Trp Ile Lys Glu Thr Met Arg Ser Lys Val Tyr Met Glu
 1   5   10   15
Gly Asp Val Asn Asn His Ala Phe Lys Cys Thr Ala Val Gly Glu Gly
            20   25   30
Lys Pro Tyr Lys Gly Ser Gln Asp Leu Thr Ile Thr Val Thr Glu Gly
        35   40   45
Gly Pro Leu Pro Phe Ala Phe Asp Ile Leu Ser His Ala Phe Gln Tyr
    50   55   60
Gly Asn Lys Val Phe Thr Asp Tyr Pro Asp Asp Ile Pro Asp Phe Phe
65   70   75   80
Lys Gln Ser Leu Ser Asp Gly Phe Thr Trp Arg Arg Val Ser Thr Tyr
                85   90   95
Asp Asp Gly Gly Val Leu Thr Val Thr Gln Asp Thr Ser Leu Lys Gly
            100   105   110
Asp Cys Ile Ile Cys Asn Ile Lys Val His Gly Thr Asn Phe Pro Glu
        115   120   125
Asn Gly Pro Val Met Gln Asn Lys Thr Asp Gly Trp Glu Pro Ser Ser
    130   135   140
Thr Glu Thr Val Ile Pro Gln Asp Gly Gly Ile Val Ala Ala Arg Ser
145   150   155   160
Pro Ala Leu Arg Leu Arg Asp Lys Gly His Leu Ile Cys His Met Glu
                165   170   175
Thr Thr Tyr Lys Pro Asn Lys Glu Val Lys Leu Pro Glu Leu His Phe
            180   185   190
His His Leu Arg Met Glu Lys Leu Ser Val Ser Asp Asp Gly Lys Thr
        195   200   205
Ile Lys Gln His Glu Tyr Val Val Ala Ser Tyr Ser Lys Val Pro Ser
    210   215   220
Lys Ile Gly Arg Gln
225

<210> 21
<211> 1030
<212> DNA
<213> Agaricia fragilis

<400> 21
caaggaagcc aaatctttta ccagagatct cgcgtgaaag caacctatga gtgatggcga 60
tttctactct aaagaacgtc atcatcatcg ttattatata ctcctgcagc acttgtgctg 120
tttggtcgaa ttcaaactct gaatcctctt tcactaatgg gattgcagag gaaatgaaga 180
ctagggtaca tttggagggt actgttaacg ggcactcctt tacaattaaa ggcgaaggaa 240
gaggctaccc ttacaaagga gaacagttta tgagccttga ggtcgtcaat ggtgctcctc 300
tgccgttctc ttttgatatc ttgacaccag catttatgta tggcaacaga gtgttcacca 360
agtacccacc aaacatacca gactatttca agcagacgtt tcctgaaggg tatcactggg 420
aaagaaacat tccctttgaa gatcaggccg cgtgcacggt aaccagccac ataagattgg 480
aagaggaaga gaggcgtttt gtaaataacg tcagatttca ctgtgtgaac tttcccccta 540
atggtccagt catgcagagg aggatactga aatgggagcc atccactgag aacatttatc 600
cgcgtgatgg gtttctggag ggccatgttg atatgactct tcgggttgaa ggaggtggct 660
attaccgagc tgagttcaaa agtacttaca aagggaagac cccagtccgc gacatgccag 720
actttcactt catagaccac cgcattgaga ttacggagca tgacgaagac tacaccaatg 780
ttgagctgca tgacgtatcc tgggctcgtt actctatgct gccgactatg taagcggaaa 840
aggcaaggca acaagacgca aaaccgccct gtttgtctct tttcataaga gatttgacaa 900
ccgtggttct ttgccattta atttgaatta gtttaaatta aatctttggg attgatgtag 960
acgctttggt tgctaagtaa gaaaacattt gtgattatta aatttgttgc ctgaagcaaa 1020
aaaaaaaaaa 1030

<210> 22
<211> 259
<212> PRT
<213> Agaricia fragilis

<400> 22
Met Ala Ile Ser Thr Leu Lys Asn Val Ile Ile Ile Val Ile Ile Tyr
 1   5   10   15
Ser Cys Ser Thr Cys Ala Val Trp Ser Asn Ser Asn Ser Glu Ser Ser
            20   25   30
Phe Thr Asn Gly Ile Ala Glu Glu Met Lys Thr Arg Val His Leu Glu
        35   40   45
Gly Thr Val Asn Gly His Ser Phe Thr Ile Lys Gly Glu Gly Arg Gly
    50   55   60
Tyr Pro Tyr Lys Gly Glu Gln Phe Met Ser Leu Glu Val Val Asn Gly
65   70   75   80
Ala Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala Phe Met Tyr
                85   90   95
Gly Asn Arg Val Phe Thr Lys Tyr Pro Pro Asn Ile Pro Asp Tyr Phe
            100   105   110
Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Asn Ile Pro Phe
        115   120   125
Glu Asp Gln Ala Ala Cys Thr Val Thr Ser His Ile Arg Leu Glu Glu
    130   135   140
Glu Glu Arg Arg Phe Val Asn Asn Val Arg Phe His Cys Val Asn Phe
145   150   155   160
Pro Pro Asn Gly Pro Val Met Gln Arg Arg Ile Leu Lys Trp Glu Pro
                165   170   175
Ser Thr Glu Asn Ile Tyr Pro Arg Asp Gly Phe Leu Glu Gly His Val
            180   185   190
Asp Met Thr Leu Arg Val Glu Gly Gly Gly Tyr Tyr Arg Ala Glu Phe
        195   200   205
Lys Ser Thr Tyr Lys Gly Lys Thr Pro Val Arg Asp Met Pro Asp Phe
    210   215   220
His Phe Ile Asp His Arg Ile Glu Ile Thr Glu His Asp Glu Asp Tyr
225   230   235   240
Thr Asn Val Glu Leu His Asp Val Ser Trp Ala Arg Tyr Ser Met Leu

245 250 255
Pro Thr Met

<210> 23
<211> 1024
<212> DNA
<213> Ricordea florida

<400> 23
agccacttcg gtgtcttgtc gagaggaagg atcacgaaca agagaagagc tgtaaaagtt 60
aaaattttac tttacttctt ccagcatgaa tgcacttcaa gaggaaatga aaatcaagct 120
tacaatggtg ggcgttgtta acgggcagtc atttaagatc gatgggaaag gaaaagggaa 180
accttacgag ggatcacagg aattgaccct taaagtggtg gaaggcgggc ctctgctctt 240
ctcttatgat atcctgacaa cgatatttca gtatggcaac agggcattcg tgaactaccc 300
aaaggacata ccagatattt tcaagcaaac gtgttctggt cttgatggcg gatattcgtg 360
gcaaaggacc atgacttatg aggacggagg ggtttgtact gctacaagca acgtcagcgt 420
ggtcggcgac actttcaatt atgaaattca ctttatgggg gcgaattttc ctccaaatgg 480
tccrgtgatg cagaaaagaa cagtgaagtg ggagccctcc actgagataa tgtttgaacg 540
tgatggattg ctgaggggtg atgttcccat gtctctgttg ctgaaaggag gcgaccatta 600
ccgatgtgac tttaaaacta tttataaacc caacaagaag gtcaagctgc caggttacca 660
ttttgtggac cactgcattg agataaagag tcaagagaat gattacaaca tggttgcgct 720
ctttgaggat gctgtagcac actactctcc tctggagaaa aagagccagg caaaggcgta 780
aatccaaaca acctaagaag acgacaaggc attcaatcta atcgcatgtt tgaatttttg 840
gttaggaatg tgttgggtca gactaggtct agaacgtttc attttggctg gatttgtttt 900
actcagttat agacaagaaa aaaatcttaa atgacttggg ttggatttag ctttcggcac 960
tgtcaattcc ggattcctta gaaatatttg agaccaagcc tttttttgag ctgagaacgt 1020
aatc 1024

<210> 24
<211> 231
<212> PRT
<213> Ricordea florida

<400> 24
Met Asn Ala Leu Gln Glu Glu Met Lys Ile Lys Leu Thr Met Val Gly
1 5 10 15
Val Val Asn Gly Gln Ser Phe Lys Ile Asp Gly Lys Gly Lys Gly Lys
20 25 30
Pro Tyr Glu Gly Ser Gln Glu Leu Thr Leu Lys Val Val Glu Gly Gly
35 40 45
Pro Leu Leu Phe Ser Tyr Asp Ile Leu Thr Thr Ile Phe Gln Tyr Gly
50 55 60
Asn Arg Ala Phe Val Asn Tyr Pro Lys Asp Ile Pro Asp Ile Phe Lys
65 70 75 80
Gln Thr Cys Ser Gly Leu Asp Gly Gly Tyr Ser Trp Gln Arg Thr Met
85 90 95
Thr Tyr Glu Asp Gly Gly Val Cys Thr Ala Thr Ser Asn Val Ser Val
100 105 110
Val Gly Asp Thr Phe Asn Tyr Glu Ile His Phe Met Gly Ala Asn Phe
115 120 125
Pro Pro Asn Gly Pro Val Met Gln Lys Arg Thr Val Lys Trp Glu Pro
130 135 140
Ser Thr Glu Ile Met Phe Glu Arg Asp Gly Leu Leu Arg Gly Asp Val
145 150 155 160
Pro Met Ser Leu Leu Leu Lys Gly Gly Asp His Tyr Arg Cys Asp Phe
165 170 175

```
Lys Thr Ile Tyr Lys Pro Asn Lys Lys Val Lys Leu Pro Gly Tyr His
            180                 185                 190
Phe Val Asp His Cys Ile Glu Ile Lys Ser Gln Glu Asn Asp Tyr Asn
        195                 200                 205
Met Val Ala Leu Phe Glu Asp Ala Val Ala His Tyr Ser Pro Leu Glu
    210                 215                 220
Lys Lys Ser Gln Ala Lys Ala
225                 230
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<210> 25
<211> 913
<212> DNA
<213> Montastraea cavernosa

<400> 25
agagctgtag ggtgatatct tacttacgtc taccatcatg accagtgttg cacaggaaaa 60
gggtgtgatt aaaccagaca tgaagatgaa gctgcgtatg gaaggtgctg taaacgggca 120
caagttcgtg attgaaggag atggaaaagg gaagcctttc gacggaacac agactatgga 180
ccttacagtc atagaaggcg caccattgcc tttcgcttac gctatcttga caacagtatt 240
cgattacggc aacagggtat tcgccaaata cccagaagac atagcagatt atttcaagca 300
gacatttcct gaggggtact tctgggaacg aagcatgaca tacgaagacc agggcatttg 360
catcgccaca aacgacataa caatgatgaa aggcgtcgac gactgttttg tctataaaat 420
tcgatttgat ggtgtgaact ttcctgccaa tggtccagtt atgcagagga agacgctgaa 480
atgggagcca tccactgaga aaatgtatgc gcgtgatgga gtgctgaagg gtgatgttaa 540
catggctctg ttgcttgaag gaggtggcca ttaccgatgt gacttcaaaa ctacttacag 600
agctaagaag gttgtccagt tgccagacta tcattttgtg gaccatcgca ttgagattgt 660
gagccacgac aaagattaca acaaggttaa gctgtatgag catgccgaag ctcattctgg 720
gctgccgagg caggccaagt aaaggcttaa tgaaaagcca agacgacaac aaggagaaac 780
aaagtatttt ttttgttaaa tttcaaggca tttactcgga attagtattt gatactttcg 840
attcaaggat ttgtttcggg acttgttaga gaccagctct agagttgtat tttgtgaaaa 900
aaagatagtt tcc 913

<210> 26
<211> 234
<212> PRT
<213> Montastraea cavernosa

<400> 26
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Met Thr Ser Val Ala Gln Glu Lys Gly Val Ile Lys Pro Asp Met Lys
 1               5                  10                  15
Met Lys Leu Arg Met Glu Gly Ala Val Asn Gly His Lys Phe Val Ile
            20                  25                  30
Glu Gly Asp Gly Lys Gly Lys Pro Phe Asp Gly Thr Gln Thr Met Asp
        35                  40                  45
Leu Thr Val Ile Glu Gly Ala Pro Leu Pro Phe Ala Tyr Ala Ile Leu
    50                  55                  60
Thr Thr Val Phe Asp Tyr Gly Asn Arg Val Phe Ala Lys Tyr Pro Glu
65                  70                  75                  80
Asp Ile Ala Asp Tyr Phe Lys Gln Thr Phe Pro Glu Gly Tyr Phe Trp
                85                  90                  95
Glu Arg Ser Met Thr Tyr Glu Asp Gln Gly Ile Cys Ile Ala Thr Asn
            100                 105                 110
Asp Ile Thr Met Met Lys Gly Val Asp Asp Cys Phe Val Tyr Lys Ile
        115                 120                 125
Arg Phe Asp Gly Val Asn Phe Pro Ala Asn Gly Pro Val Met Gln Arg
    130                 135                 140
Lys Thr Leu Lys Trp Glu Pro Ser Thr Glu Lys Met Tyr Ala Arg Asp
```

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145                 150                 155                 160
Gly Val Leu Lys Gly Asp Val Asn Met Ala Leu Leu Leu Glu Gly Gly
                165                 170                 175
Gly His Tyr Arg Cys Asp Phe Lys Thr Thr Tyr Arg Ala Lys Lys Val
            180                 185                 190
Val Gln Leu Pro Asp Tyr His Phe Val Asp His Arg Ile Glu Ile Val
        195                 200                 205
Ser His Asp Lys Asp Tyr Asn Lys Val Lys Leu Tyr Glu His Ala Glu
    210                 215                 220
Ala His Ser Gly Leu Pro Arg Gln Ala Lys
225                 230
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<210> 27
<211> 1133
<212> DNA
<213> Montastraea annularis

<400> 27
tggttaacgc agagtcgcgg ggggttcctg gctaataatt gattctattt tgggtgtgac 60
attcaggttt aaagcagcat cctcagtgct gaggtctcat tcaccctggt gatttggaag 120
agagcagatc gagaacacca agagctgtat tacgctaaaa tcttacttgc ctctaccacc 180
atgagtatga ttaaaccaga aatgaagatc aagatgcgta tggacggtgc tgtaaacggg 240
cacaagttcg tgattacagg ggaaggaagc ggcgagcctt tcgagggaaa acagactatg 300
aacctgacag tcatagacgg cggacctctg cctttcgctt tcgacatctt gacaacagca 360
ttcgattacg gcamcagggt attcgccaaa tacccagaag acatcccaga ctatttcaag 420
cagtcgtttc ctgaggggtt ttcttgggaa cgaagcatga cttacgaaga cgggggcatt 480
tgcatcgcca caaatgacat aaaaatggaa ggcgactgct tttcctatga aattcgattt 540
gatggggtga actttcctgc caatagtcca gttatgcaga agaagaccgt gaaatgggag 600
ccatgcactg rggaaatgta tgtgcgtgat ggagtgctta aaggtggtct taacatggct 660
ctgttgcttg aaggaggtgg ccatttccga tgtgacttga aaactactta caaagctaag 720
aaggttgtcc agatgccaga ctatcacttt gtgaatcacc gacttgagat aacatggcat 780
gacgaggatt acaacaatgt taagctgtct gagcatgcag aagctcattc tggactgcca 840
aggcaggcca aataaaggct tgacgaaaag ccaaaacggc aaagagtaca agaaagtata 900
tataaatgta tatttttcaa ctgaaaggca ttccactcgg aattagtatt tgatactttc 960
aattcaagga tttattttgg gatttgctag ccactagctt tattgttaaa ttaagttaaa 1020
gacggtttag catttttcg gtattacaac ataggcacag acgtcttaac cccagtagtg 1080
gtcaggtaca agtaagaaaa ctttggtgag aatagacttg tagtcgaaaa aaa 1133

<210> 28
<211> 224
<212> PRT
<213> Montastraea annularis

<220>
<221> VARIANT
<222> 65, 144
<223> Xaa = Any Amino Acid

<400> 28
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Met Ser Met Ile Lys Pro Glu Met Lys Ile Lys Met Arg Met Asp Gly
 1               5                  10                  15
Ala Val Asn Gly His Lys Phe Val Ile Thr Gly Glu Gly Ser Gly Glu
            20                  25                  30
Pro Phe Glu Gly Lys Gln Thr Met Asn Leu Thr Val Ile Asp Gly Gly
        35                  40                  45
Pro Leu Pro Phe Ala Phe Asp Ile Leu Thr Thr Ala Phe Asp Tyr Gly
    50                  55                  60
```

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Xaa Arg Val Phe Ala Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Phe Lys
65                  70                  75                  80
Gln Ser Phe Pro Glu Gly Phe Ser Trp Glu Arg Ser Met Thr Tyr Glu
                85                  90                  95
Asp Gly Gly Ile Cys Ile Ala Thr Asn Asp Ile Lys Met Glu Gly Asp
            100                 105                 110
Cys Phe Ser Tyr Glu Ile Arg Phe Asp Gly Val Asn Phe Pro Ala Asn
        115                 120                 125
Ser Pro Val Met Gln Lys Lys Thr Val Lys Trp Glu Pro Cys Thr Xaa
    130                 135                 140
Glu Met Tyr Val Arg Asp Gly Val Leu Lys Gly Gly Leu Asn Met Ala
145                 150                 155                 160
Leu Leu Leu Glu Gly Gly Gly His Phe Arg Cys Asp Leu Lys Thr Thr
                165                 170                 175
Tyr Lys Ala Lys Lys Val Val Gln Met Pro Asp Tyr His Phe Val Asn
            180                 185                 190
His Arg Leu Glu Ile Thr Trp His Asp Glu Asp Tyr Asn Asn Val Lys
        195                 200                 205
Leu Ser Glu His Ala Glu Ala His Ser Gly Leu Pro Arg Gln Ala Lys
    210                 215                 220
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